PhytoKeys 259: 161–175 (2025)
DOI: 10.3897/phytokeys.259.156141

Research Article

Synotis lhozhagensis (Asteraceae, Senecioneae), a new species from south-eastern Xizang, China, based on morphological and molecular evidence

Guo-Xing Peng[1*], Liao-Cheng Zhao[2*], Ming Tang[1,3,4], Jun Deng[1], Hao-Ming Zhan[1], Zhuo-Ni Zhang[1], Qiang Wang[5,6,7]

1 *College of Forestry, Jiangxi Agricultural University, Nanchang 330045, Jiangxi, China*
2 *Laboratory of Systematic Evolution and Biogeography of Woody Plants, College of Ecology and Nature Conservation, Beijing Forestry University, Beijing, 10083, China*
3 *Jiangxi Provincial Key Laboratory of Improved Variety Breeding and Efficient Utilization of Native Tree Species, Jiangxi Agricultural University, Nanchang 330045, Jiangxi, China*
4 *Jiangxi Provincial Key Laboratory of Conservation Biology, Jiangxi Agricultural University, Nanchang 330045, Jiangxi, China*
5 *State Key Laboratory of Plant Diversity and Specialty Crops, Institute of Botany, Chinese Academy of Sciences, Beijing 100093, China*
6 *National Botanical Garden, Institute of Botany, Chinese Academy of Sciences, Beijing 100093, China*
7 *College of Life Sciences, University of Chinese Academy of Sciences, Beijing 100049, China*
Corresponding author: Ming Tang (tangming@jxau.edu.cn)

Abstract

Synotis lhozhagensis, a new species belonging to Senecioneae (Asteraceae), is described and illustrated herein after being discovered during biodiversity surveys in Lhozhag County, Xizang Autonomous Region, China. This species is similar to *S. acuminata* (Wall. ex DC.) C.Jeffrey & Y.L.Chen, but differs mainly in having the ray floret absent (vs. 1), the leaf margins irregularly coarsely serrate (vs. finely mucronulate-serrate) and the phyllaries five (vs. three or four). It is also allied to *S. glomerata* C.Jeffrey & Y.L.Chen in growth habit, leaf blade morphology and inflorescence structure, but is distinguished by the corymbs loose and spreading (vs. dense and glomeruliform), the ligulate floret absent (vs. one or two) and the disc florets five (vs. three or four). Phylogenetic analysis, based on ITS sequences, confirms its distinct taxonomic status within *Synotis*. A line drawing and colour plates, a geographic distribution map, a detailed comparison table including the aforementioned three species and the provisional IUCN status are provided.

Key words: Compositae (Asteraceae), morphology comparison, phylogenetic analysis, taxonomy, Xizang (Tibet)

OPEN ACCESS

Academic editor: Gianmarco Tavilla
Received: 17 April 2025
Accepted: 28 May 2025
Published: 1 July 2025

Citation: Peng G-X, Zhao L-C, Tang M, Deng J, Zhan H-M, Zhang Z-N, Wang Q (2025) *Synotis lhozhagensis* (Asteraceae, Senecioneae), a new species from south-eastern Xizang, China, based on morphological and molecular evidence. PhytoKeys 259: 161–175. https://doi.org/10.3897/phytokeys.259.156141

Copyright: © Guo-Xing Peng et al.
This is an open access article distributed under terms of the Creative Commons Attribution License (Attribution 4.0 International – CC BY 4.0).

Introduction

Synotis (C.B. Clarke) C. Jeffrey & Y.L. Chen (Asteraceae, Senecioneae), a genus endemic to the Central Himalayas (Jeffrey and Chen 1984; Nordenstam 2007; Tang et al. 2013a, b; Tang 2014; Tong et al. 2017; Zhao et al. 2023; Jin et al. 2024; Liu et al. 2024), comprising approximately 62 species primarily distributed in the Sino-Himalayayan Region. Southwest China serves as its centre of

* These authors contributed equally to this work.

diversity, hosting over 50 documented species (Chen et al. 2011; Tang 2014; Liu et al. 2021; Fan et al. 2022; Liu et al. 2024). Despite the foundational taxonomic framework established by Jeffrey and Chen (1984) through comprehensive revisions, species delimitation within this genus remains challenging due to the high uniformity of morphological traits (Tong et al. 2017; Liu et al. 2024). Tang (2014) conducted an integrative taxonomic study combining morphological analyses (including ultrastructural observations via scanning electron microscopy, SEM), cytological data and molecular phylogenetics on the genus and refined the subordinate taxonomic system, pointed out the five series belonging to two sections, i.e. sect. *Synotis* and sect. *Atractylidifoliae* C. Jeffrey & Y. L. Chen, were included in the genus. Li et al. (2018) transferred *Senecio karelinioides* C. Winkl. to *Synotis* based on evidence from morphology, karyology and ITS/ETS sequence data and recombined *Sen. karelinioides* as *Syn.* sect. *Karelinioidei* (O. Fedtsch. & B. Fedtsch. ex Schischk.) C. Ren, Lazkov & I. D. Illar., treating *Synotis* sect. *Atractylidifoliae* as a synonym of the new combination.

During biodiversity surveys conducted in Lhozhag County, Xizang Autonomous Region in August 2024, we discovered a morphologically distinct population of *Synotis* near Lakang Town. Initial morphological comparisons showed that its leaf characteristics were congruent with *S. acuminata*, whereas its floral traits (smaller capitula with five phyllaires) were more aligned with *S. glomerata*. Subsequent targeted morphological examinations, along with molecular phylogenetic analyses using ITS sequence data, confirmed the phylogenetic distinctiveness of the taxon within the genus. We hereby formally describe this previously undocumented species as *Synotis lhozhagensis* sp. nov., with its systematic placement resolved through integrative taxonomic assessment.

Material and methods

Morphological analyses

Field observations of the natural habitat and habit of the new taxon were systematically recorded. Comparative studies of the new species and its putative allies were conducted by field observation and examination of specimens, focusing on diagnostic characters: leaf and inflorescence shape, capitula size, number of phyllaries and presence or absence of ray florets. Key morphological traits of five specimens were documented using a standardised digital imaging system (Olympus TG-6) according to the protocols of Zhao et al. (2023).

Species sampling, DNA extraction and sequencing

Based on previous phylogenetic studies in Senecioneae (Pelser et al. 2007, 2010; Zhao et al. 2023; Jin et al. 2024), we selected 43 samples encompassing 41 species and one subspecies, across seven genera, including 14 *Synotis* and 23 *Senecio* taxa, with *Abrotanella emarginata* Cass. (subtribe Abrotanellinae) chosen as the outgroup.

Furthermore, we generated new sequences for the newly-discovered species (vouchers.01/02) using the modified CTAB method (Doyle and Doyle 1987). Low-coverage genomic data (> 2 Gb per sample) were obtained through Illumina

NovaSeq PE150 sequencing (Novogene, Beijing), employing library preparation following a 150 bp paired-end strategy. Raw sequencing data were processed using Trimmomatic v. 0.39 (Bolger et al. 2014) to remove unpaired and low-depth reads, enhancing the accuracy and quality of the assembly. Filtered data were assembled into nuclear ribosomal DNA (nrDNA) sequences using GetOrganelle v. 1.7.7(Jin et al. 2020) and ITS sequence was extracted from nrDNA sequence with ITSx (Bengtsson et al. 2013).

In addition to sequencing the newly-described species, nuclear ribosomal (ITS) regions of its putative relatives, *S. glomerata* and *S. acuminata*, were amplified using the ITS4 and ITS5 primer pairs (White et al. 1990) following the protocols of Tang (2014). ITS sequences of the remaining species were retrieved from the GenBank database. Voucher information and GenBank accession numbers for the material used in this study are provided in Appendix 1 (Table A1).

Phylogenetic analyses

Data processing and analysis were performed using PhyloSuite v.1.2.3 (Zhang et al. 2020). Multiple sequence alignment was carried out with MAFFT v.7 (Katoh and Standley 2013). Maximum Likelihood (ML) inference was conducted in IQ-TREE v.2.2.0 (Nguyen et al. 2015) under the SYM+G4 model, selected by ModelFinder (Kalyaanamoorthy et al. 2017), based on the corrected Bayesian Information Criterion. Node support was derived from 1,000,000 ultrafast bootstrap replicates (Minh et al. 2013). Bayesian Inference (BI) was executed using MrBayes v.3.2.7 (Ronquist et al. 2012) under the SYM+G4 model, with two independent runs of 2,000,000 generations each, sampling every 1,000 generations. Convergence was assessed by monitoring the average standard deviation of split frequencies (< 0.01) and ensuring effective sample sizes (ESS) exceeded 200 for all parameters. After discarding the initial 25% of samples as burn-in, posterior probabilities (PP) were calculated from the remaining trees. Bootstrap percentage (MLBS) values ≥ 70 (Huelsenbeck et al. 1993) and PP values ≥ 0.90 (Leaché et al. 2002) were considered strong support. Finally, the phylogenetic trees were visualised using FigTree v.1.4.

Results and discussion

General morphology

Synotis lhozhagensis closely resembles *S. glomerata* and *S. acuminata* morphologically, but is distinguished by a suite of macroscopic morphological traits: *S. lhozhagensis* is relatively taller (100–250 cm vs. 40–150 cm in *S. acuminata* and ≤ 120 cm in *S. glomerata*), leaves with irregularly deep obtuse-acuminate serrate margins (vs. remotely mucronate-serrulate margins in *S. acuminata* and *S. glomerata*), capitula lacks ray florets (vs. one in *S. acuminata* and one or two in *S. glomerata*), disc florets five (vs. two or three in *S. acuminata* and three or four in *S. glomerata*) (Figs 1, 6, 7, Table 1). These differences highlight *S. lhozhagensis* as a unique taxon within the genus.

Table 1. Morphological comparison of *Synotis lhozhagensis* sp. nov., *S. glomerata* and *S. acuminata*.

Character	*Synotis lhozhagensis*	*S. glomerata*	*S. acuminata*
Stem	100–250 cm tall, white-tomentose when young	≤ 120 cm tall, yellowish-brown tomentose	40–150 cm tall, yellowish-brown pubescent
Leaf size	6–13 × 1.5–3 cm	6–22 × 1.5–6 cm	8–18 × 1.5–3.5 cm
Leaf margin	Irregularly serrate-dentate	Finely serrulate with mucronate teeth	Sparsely serrulate
Lateral veins	4–6 pairs	8 or 9 pairs	5 or 6 pairs
Inflorescence type	Loose thyrsoid-paniculate	Dense globose corymb (20–25 capitula)	Compound corymb
Phyllaries	5, oblong, silvery-puberulent	5, oblong, apex obtuse	3 or 4, linear-oblong, glabrous
Ray florets	Absent	1 or 2, corolla liliform, 3–5 mm long	1, corolla linear, 5–7 mm long
Disc florets	5, pale yellow, corolla 8 mm long	3 or 4, yellow, corolla 7 mm long	2 or 3, yellow, corolla 7 mm long

Phylogenetic analyses

Both Maximum Likelihood (ML) and Bayesian Inference (BI) phylogenetic analyses yield congruent topologies, with the ML tree topology being presented here (Fig. 4). The genus *Synotis* formed a strongly supported monophyletic clade (MLBS = 99, PP = 1.00), consistent with previous phylogenetic studies (Pelser et al. 2007, 2010; Tang et al. 2014; Tong et al. 2017; Li et al. 2018; Zhao et al. 2023; Jin et al. 2024). The newly-described species *S. Lhozhagensis* was regarded as a strongly supported monophyletic lineage (MLBS = 100, PP = 1.00) with its congener *S. acuminata*, confirming its taxonomic distinctiveness (MLBS = 96, PP = 0.99).

Taxonomic treatment

***Synotis lhozhagensis* M.Tang, sp. nov.**
urn:lsid:ipni.org:names:77364872-1
Figs 1–3

Chinese name. "luò zā hé ěr jú" (洛扎合耳菊)

Type. China • Xizang Autonomous Region, Shannan City, Lhozhag County, Lakang Town, in fertile loamy soils at the edge of forests, 28°02'41.75"N, 91°05'50.97"E, 2720.7 m elev., 23 August 2024, FLPH Expedition 24-14847 (holotype, PE!; isotype, JXAU! PE!). Fig. 2.

Diagnosis. *Synotis lhozhagensis* is similar to *S. acuminata*, but differs in having phyllaries number five (vs. three or four), ray floret absent (vs. one) and disc florets five (vs. two or three).

Description. Perennial herbs. Stem solitary, erect, 100–250 cm tall, slightly curved distally, profusely branched into short inflorescence branches, white-tomentose when young, becoming glabrous with age. Leaves papery, long-elliptic to oblanceolate-elliptic, 6–13 cm long, 1.5–3 cm wide; apex long-acuminate; base cuneate to attenuate; margins irregularly deeply obtuse-acuminate-serrate; adaxial surface sparsely adnate white-tomentose to nearly glabrous; abaxial surface sparsely white-tomentose; venation pinnate with 4–6 pairs of lateral veins, arcuately ascending; petiole 5–15 mm long, sparsely white-tomentose to nearly glabrous. Capitula lacking ray florets, aggregated into cymose panicles; peduncles short, 3–6 mm long,

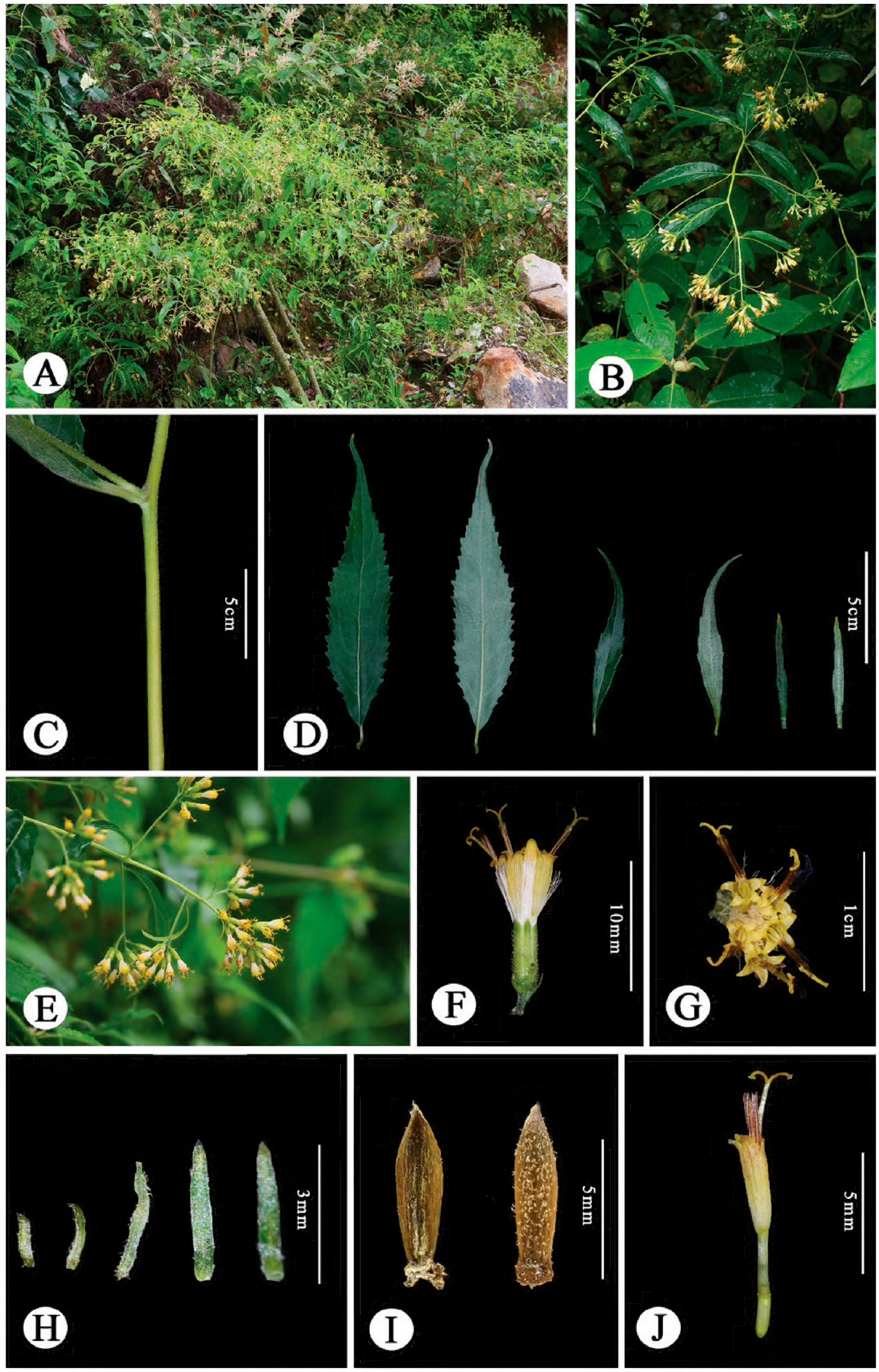

Figure 1. *Synotis lhozhagensis* in its natural habitat in Shannan, Xizang, China. **A.** Habitat; **B.** Habit; **C.** Portion of stem (sparsely tomentose); **D.** Leaf blades (left one and two: adaxial surface and abaxial surface; left three and left four: adaxial surface and abaxial surface; left five and left six: adaxial surface and abaxial surface); **E.** Synflorescence; **F.** Capitulum, lateral view; **G.** Capitulum, apical view; **H.** Outer phyllaries (= bracts of calyculus); **I.** Phyllary, adaxial (left) and (right) surfaces; **J.** Disc floret. Photographed by H.L. Zheng & X.T. Ma.

Figure 2. Holotype sheet of *Synotis lhozhagensis*. Lakang, Lhozhag, Shannan, Xizang, China, *FLPH Expedition 24-14847* (PE).

silvery-white-tomentose, bearing 1–2 basal bracts and bracteoles; bracts and bracteoles linear. Involucre terete, 4–5 mm long, 1.5–2 mm wide; bracts of calyculus 4–5, linear-subulate, up to 1/3 the length of involucre; involucral phyllaries five, oblong, 1.5 mm wide, apex acute, subleathery, margins broadly scarious, abaxially sparsely silvery-white pubescent. Disc florets

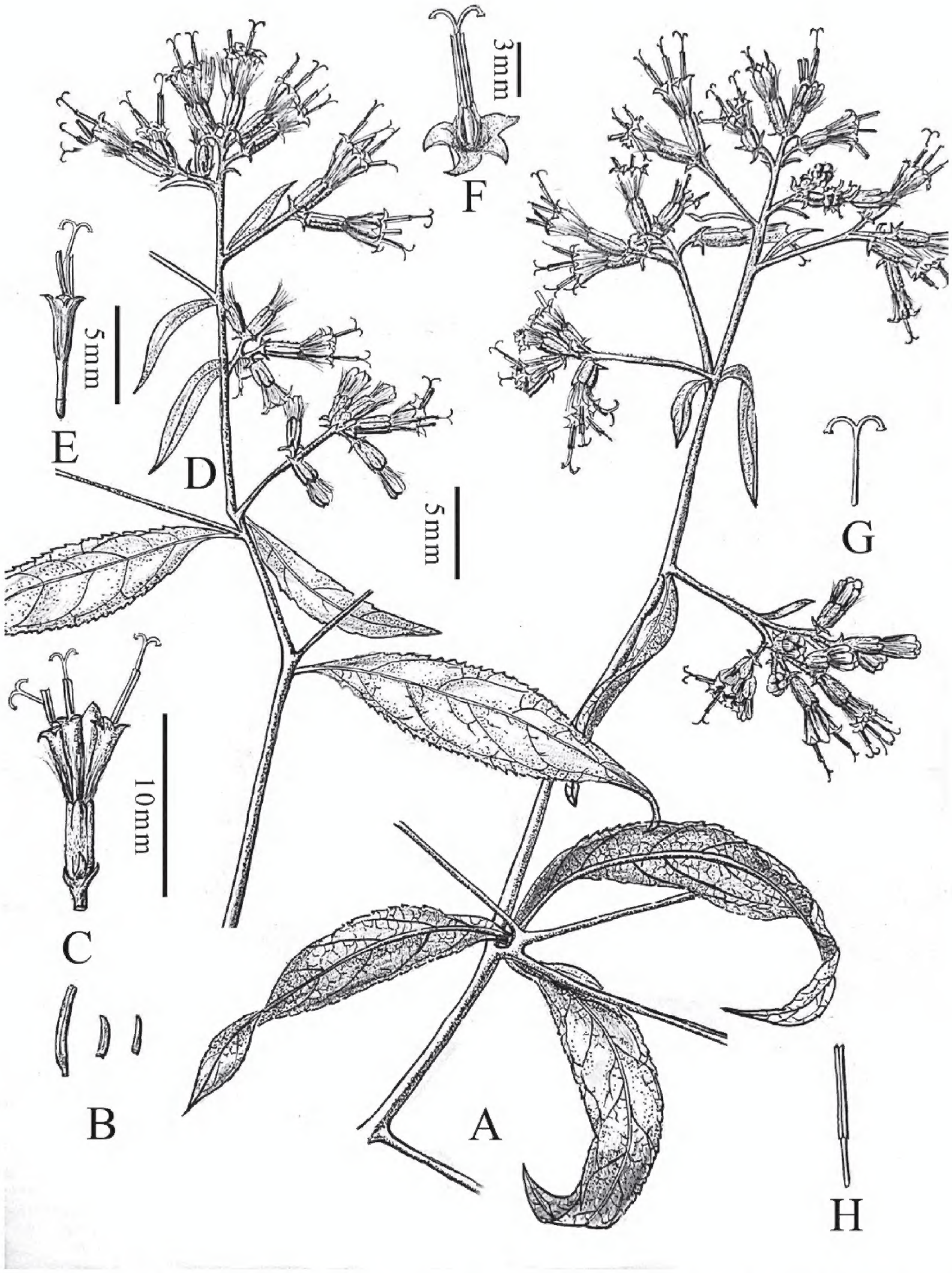

Figure 3. Line drawing of *Synotis lhozhagensis*. **A.** Habit; **B.** Outer phyllaries (bracts of calyculus); **C.** Capitula; **D.** Synflorescence; **E.** Disc floret; **F.** Corolla; **G.** Style; **H.** Stamen. Illustration by Guo-Xing Peng based on living field-collected material (*FLPH Expedition 24-14847*).

five; corolla pale yellow, ca. 6–8 mm long; tube 2.5 mm long; limb funnel-form; Style branches 1–1.2 mm long, apically obtuse, covered with short papillate hairs, central hairs inconspicuous. Achenes cylindrical, 2.5 mm long, glabrous. Crown hairs 5 mm long, white.

Phenology. Flowering July to August; fruiting September to October.

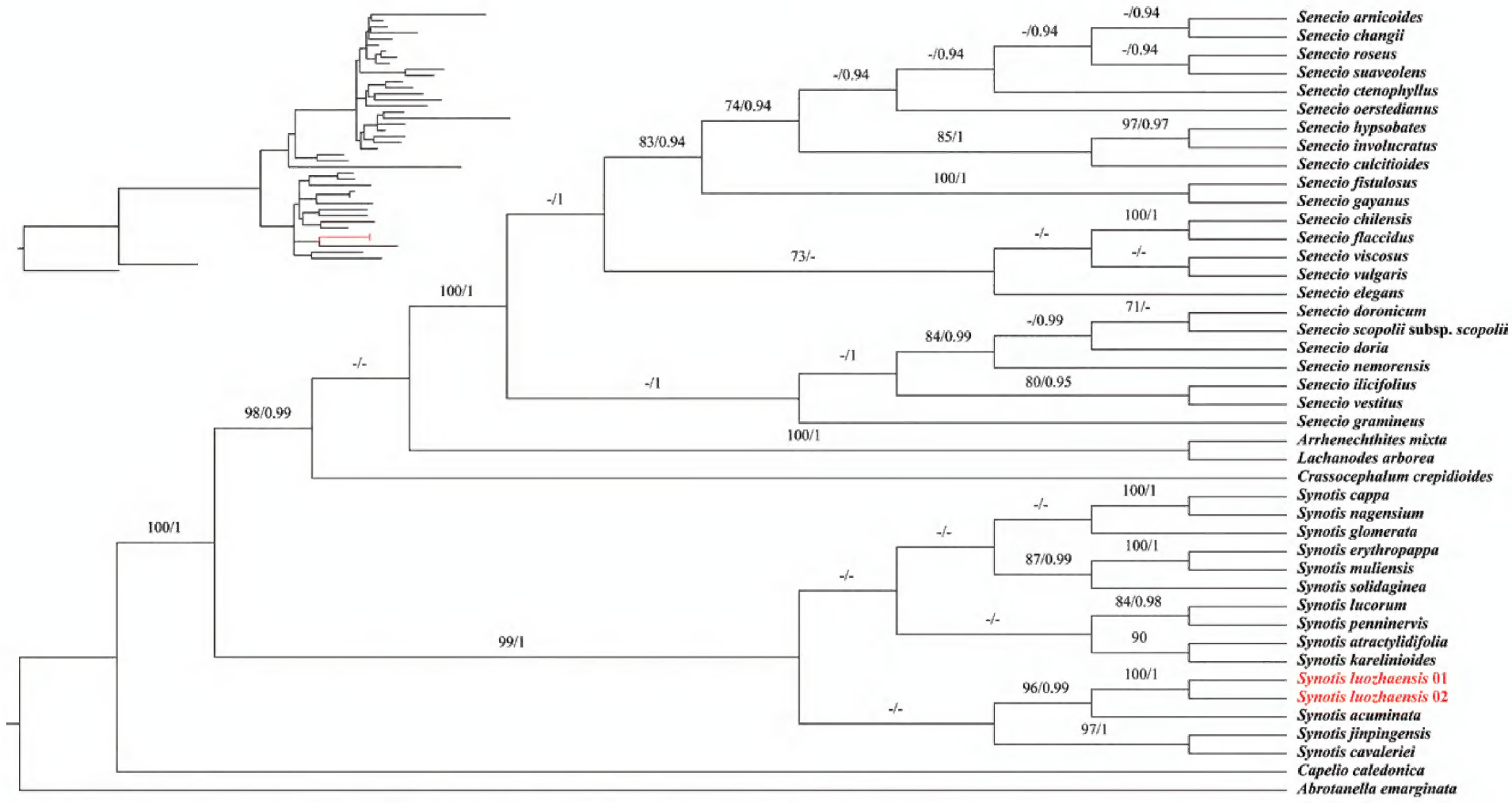

Figure 4. Maximum Likelihood tree for the Senecioneae based on the ITS dataset, with *Synotis lhozhagensis* highlighted in red font. Bootstrap values (MLBS) and posterior probabilities (PP) are indicated above the branches. Dashes (–) indicate MLBS < 70 or PP < 0.90.

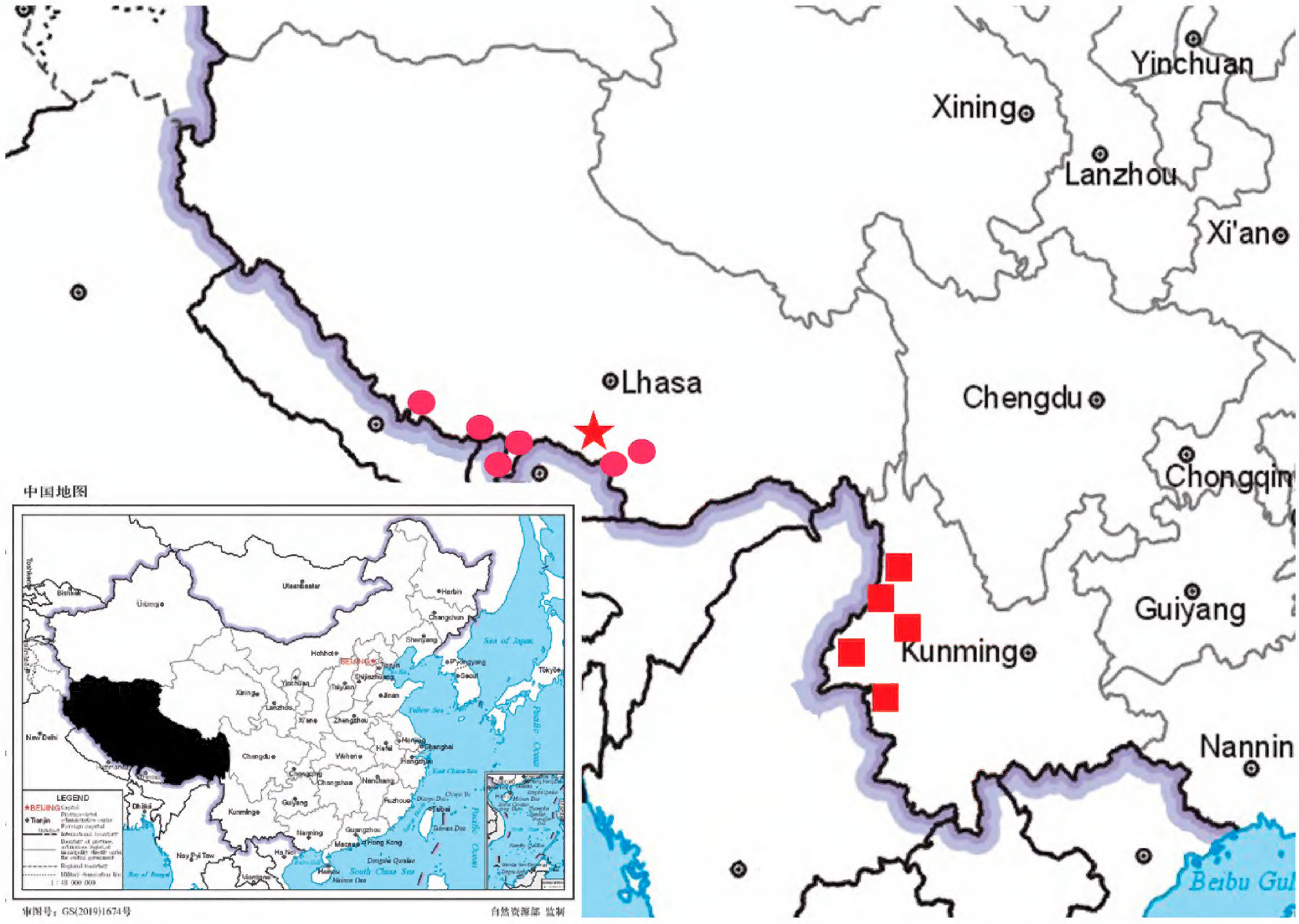

Figure 5. Distribution map of *Synotis lhozhagensis* (red pentacle), *Synotis acuminata* (red round) and *Synotis glomerata* (red square block).

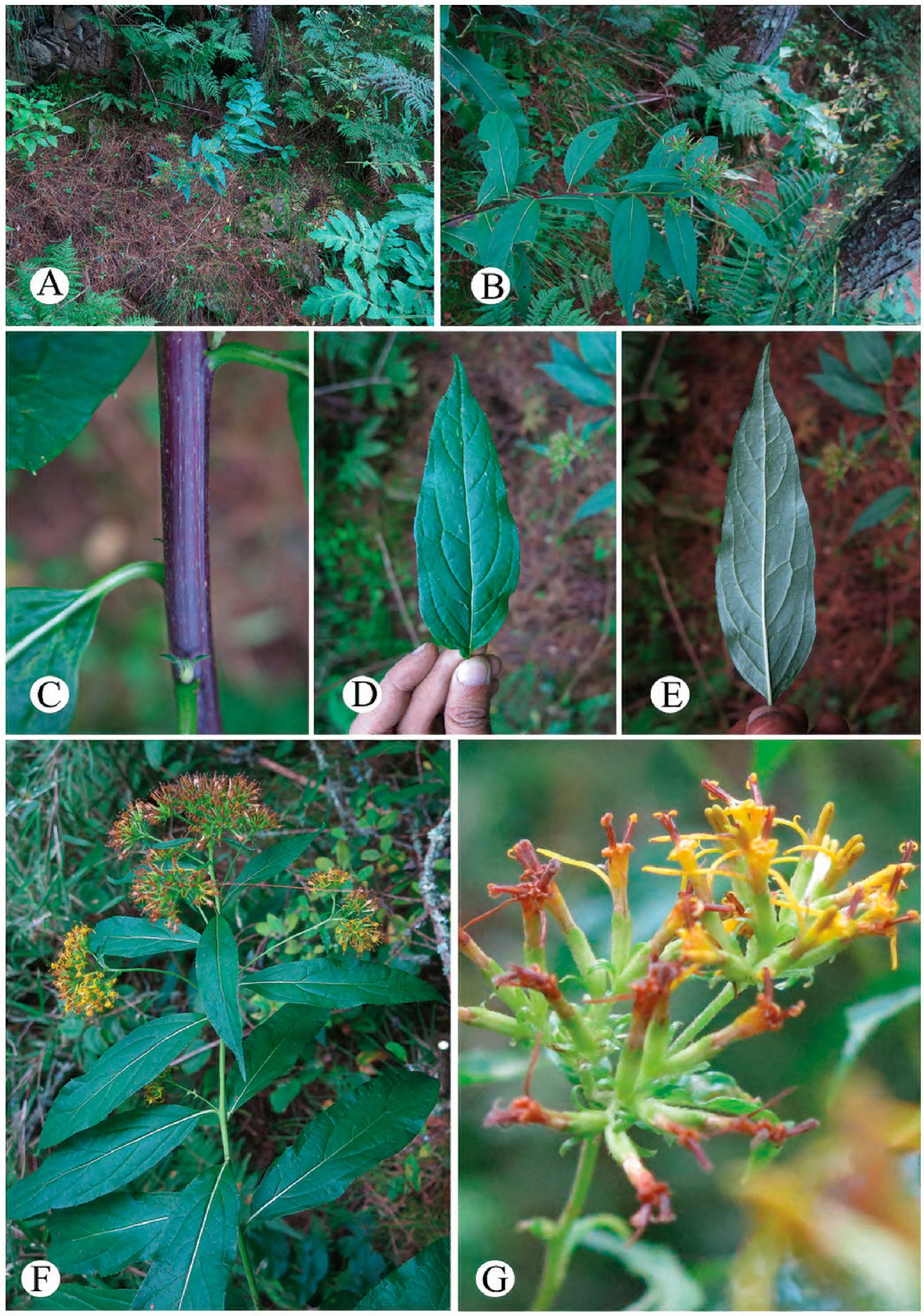

Figure 6. *Synotis acuminata* in the wild (Shannan, Xizang, China) **A.** Habitat; **B.** Habit; **C.** Portion of stem (sparsely tomentose); **D.** Leaf blade adaxial surface; **E.** Leaf blade abaxial surface; **F.** Synflorescence; **G.** Flowers (top view). Photographed by M. Tang.

Etymology. The specific epithet '*lhozhagensis*' is derived from the type locality, Lakang Town, Lhozhag County, Shannan City, southeast Xizang Autonomous Region, China.

Distribution and habitat. *Synotis lhozhagensis* is currently known only from Lakang Town, Lhozhag County, Shannan City, Xizang Autonomous Region, China. This species inhabits forest edges and sparse understorey areas, primarily within mixed forests at elevations between 2,500 and 3,000 m (Fig. 5).

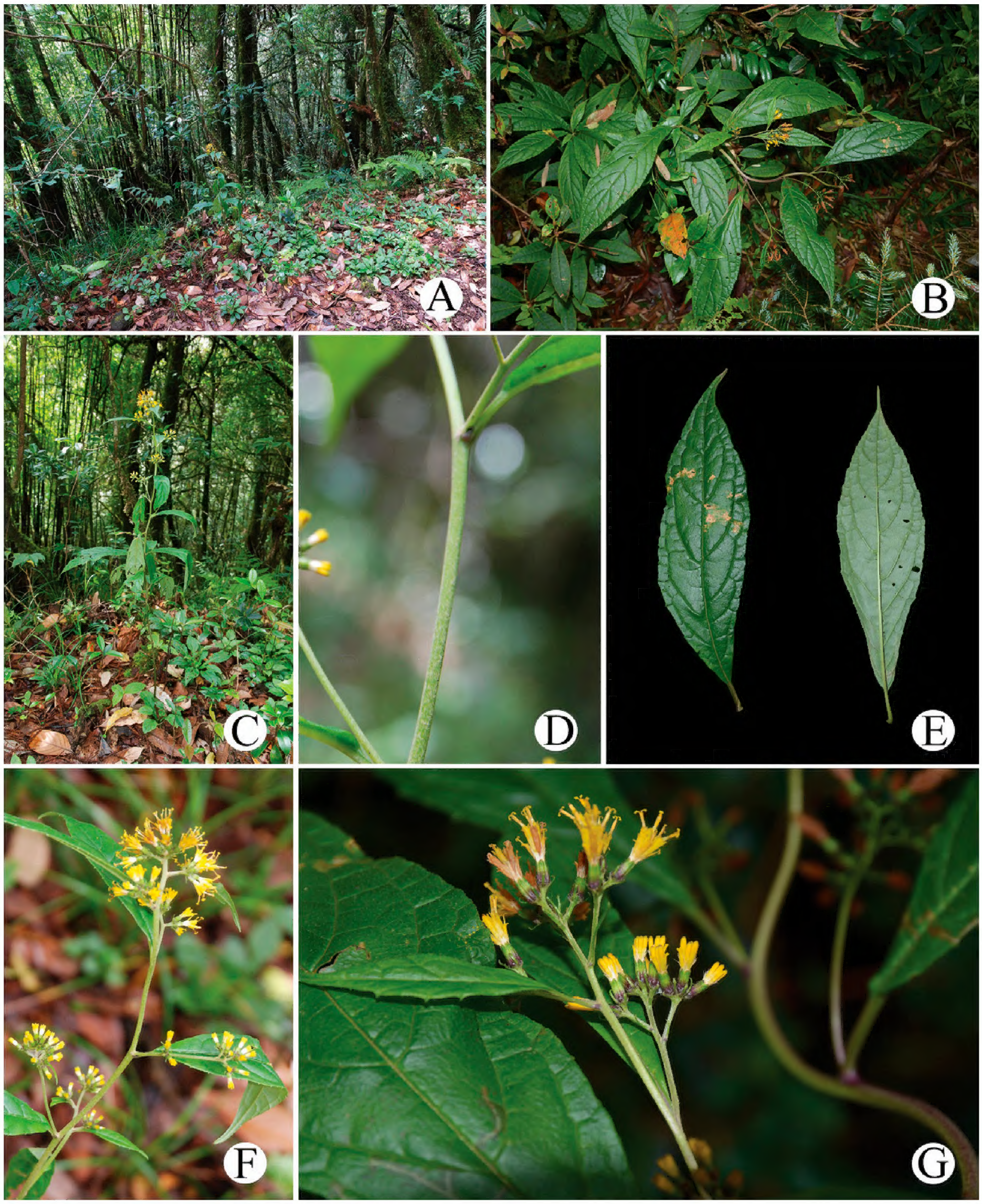

Figure 7. *Synotis glomerata* in the wild (Yuxi, Yunnan, China) **A.** Habitat; **B.** Habit; **C.** Habit; **D.** Portion of stem (sparsely tomentose); **E.** Adaxial (left) and abaxial (right) sides of leaf blade; **F.** Synflorescence; **G.** Flowers (top view). All photographed by M. Tang, except B, G by Y. Yang.

IUCN Red List Category. *Synotis lhozhagensis* is currently known only from its type locality near Lakang Town, Lhozhag County, Xizang Autonomous Region, China. Several small populations (with a total of no more than 100 plants) occur on forested hillsides within this area, thriving in well-preserved

habitats with minimal anthropogenic disturbance. Following the IUCN Red List Categories and Criteria (IUCN 2022), we propose a provisional assessment of Data Deficient (DD) for this species, as it is newly described and additional populations may remain undiscovered.

Additional specimens of *Synotis lhozhagensis* examined. Xiongqu River Valley, La Jiao Village, Lhozhag County, Xizang, 2751 m elev., 28°03'07.30"N, 91°05'25.88"E, 17 August 2013, *Y.S. Chen et al. 13-1370* (PE01992899!, PE01992904!, PE01992905!).

Note. It is noteworthy that, due to the insufficient number of samples within *Synotis*, the systematic position of *Synotis lhozhagensis* within *Synotis* has not been well resolved in the phylogenetic tree (Fig. 4). However, since the new species has loose corymbs that bear no ray florets, it can be easily placed under ser. *Oliganthae* (J.F.Jeffrey) C.Jeffrey & Y.L.Chen according to Chen et al. (2011) and Tang (2014).

During our specimen review, we characterised a novel population of particular interest, i.e. *S. Noshiro et al. 9830074* (BM000810806!, E00226303!, TI!) collected in Sankhuwasabha District, Koshi Zone, Nepal on 20 August 1998, which closely matches *Synotis lhozhagensis* in key features, such as plant form, leaf shape and flower clusters. However, they differ by having only two or three phyllaries. Further research is needed to confirm whether these specimens are the same as *Synotis lhozhagensis* or represent another new taxon never described.

Acknowledgements

We are grateful to Jiangxi Provincial Key Laboratory of Improved Variety Breeding and Efficient Utilization of Native Tree Species, Jiangxi Agricultural University (20232198405231870) for its good scientific experimental platform for the success of our work. We also thank Dr. Gianmarco Tavilla and the anonymous reviewers who gave insightful comments for the improvements of our manuscript, Dr. Yousheng Chen from South China Botanical Garden, Chinese Academy of Sciences, for providing the information about the collection site of the new species, Dr. Xintang Ma from Institute of Botany, Chinese Academy of Sciences and Dr. Hailei Zheng from Wild Dali Nature Education and Research Center, for their great help in the field and Dr. Yi Yang for his permission for using two images of *Synotis glomerata*. Thanks also go to the curators of the Herbaria of BM, E, GZTM, IBSC, KUN, LBG, PE and TI for allowing us to examine and use their scanned images of specimens.

Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Funding

This work was supported by the Survey of Wildlife Resources in Key Areas of Xizang (Phase II) (Grant No. ZL202203601 & ZL202303601) and the Science & Technology Fundamental Resources Investigation Program (Grant No.2022FY202200).

Author contributions

Data curation: GXP, LCZ, MT. Funding acquisition: MT, QW. Investigation: MT, XTM, HLZ. Methodology: GXP, LCZ, JD, MT. Project administration: MT. Supervision: MT, QW. Visualisation: GXP, ZNZ, HMZ. Writing–original draft: GXP, LCZ, MT. Writing–review and editing: GXP, MT.

Author ORCIDs

Guo-Xing Peng https://orcid.org/0009-0003-9109-0282
Liao-Cheng Zhao https://orcid.org/0000-0002-6300-7301
Ming Tang https://orcid.org/0000-0001-8419-0996
Jun Deng https://orcid.org/0009-0002-5539-0408
Hao-Ming Zhan https://orcid.org/0009-0008-2996-6040
Zhuo-Ni Zhang https://orcid.org/0009-0004-6584-0673
Qiang Wang https://orcid.org/0000-0002-0699-2034

Data availability

All of the data that support the findings of this study are available in the main text.

References

Bengtsson PJ, Ryberg M, Hartmann M, Branco S, Wang Z, Godhe A, De Wit P, Sánchez-García M, Ebersberger I, de Sousa F, Amend A, Jumpponen A, Unterseher M, Kristiansson E, Abarenkov K, Bertrand YJK, Sanli K, Eriksson KM, Vik U, Veldre V, Nilsson RH (2013) Improved software detection and extraction of ITS1 and ITS 2 from ribosomal ITS sequences of fungi and other eukaryotes for analysis of environmental sequencing data. Methods in Ecology and Evolution 4(10): 914–919. https://doi.org/10.1111/2041-210X.12073

Bolger AM, Lohse M, Usadel B (2014) Trimmomatic. A flexible trimmer for Illumina sequence data. Bioinformatics (Oxford, England) 30(15): 1–7. https://doi.org/10.1093/bioinformatics/btu170

Chen YL, Nordenstam B, Jeffrey C (2011) *Synotis* (C.B. Clarke) C.Jeffrey & Y.L. Chen. In: Wu ZY, Raven PH, Hong DY (Eds) Flora of China (Vols 20–21). Science Press, Beijing & Missouri Botanical Garden Press, St. Louis, 489–505.

Doyle JJ, Doyle JL (1987) A rapid DNA isolation procedure for small quantities of fresh leaf tissue. Phytochemical Bulletin 19(1): 11–15. https://doi.org/10.1016/0031-9422(80)85004-7

Fan Y, Zhang R, Guo CL, Tang M (2022) On the identity of Synotis ionodasys (Asteraceae: Senecioneae) from Yunnan, China. Phytotaxa 545(2): 207–216. https://doi.org/10.11646/phytotaxa.545.2.9

Huelsenbeck JP, Hilis DM (1993) Success of phylogenetic methods in the four-taxon case. Systematic Biology 42(3): 247–264. https://doi.org/10.1093/sysbio/42.3.247

IUCN (2022) Guidelines for Using the IUCN Red List Categories and Criteria. Version 15. Prepared by the Standards and Petitions Committee. http://www.iucnredlist.org/documents/RedListGuidelines.pdf

Jeffrey C, Chen YL (1984) Taxonomic studies on the tribe Senecioneae (Compositae) of Eastern Asia. Kew Bulletin 39(2): 205–446. https://doi.org/10.2307/4110124

Jin JJ, Yu WB, Yang JB, Song Y, DePamphilis CW, Yi TS, Li DZ (2020) GetOrganelle: A fast and versatile toolkit for accurate de novo assembly of organelle genomes. Genome Biology 21: 1–31. https://doi.org/10.1101/256479

Jin Z, Song Z, Guo Y, Chen Y (2024) *Synotis carnosifolia* (Asteraceae, Senecioneae), a new species from Yunnan,China. Phytotaxa 660(2): 171–180. https://doi.org/10.11646/phytotaxa.660.2.7

Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermiin LS (2017) ModelFinder: Fast model selection for accurate phylogenetic estimates. Nature Methods 14(6): 587–589. https://doi.org/10.1038/nmeth.4285

Katoh K, Standley DM (2013) MAFFT multiple sequence alignment software version 7: Improvements in performance and usability. Molecular Biology and Evolution 30(4): 772–780. https://doi.org/10.1093/molbev/mst010

Leaché AD, Reeder TW (2002) Molecular systematics of the eastern fence lizard (Sceloporus undulatus): A comparison of parsimony, likelihood, and Bayesian approaches. Systematic Biology 51(1): 44–68. https://doi.org/10.1080/106351502753475871

Li HM, Lazkov GA, Illarionova ID, Tong TJ, Shao YY, Ren C (2018) Transfer of *Senecio karelinioides* (Asteraceae, Senecioneae) to *Synotis* based on evidence from morphology, karyology and ITS/ETS sequence data. Nordic Journal of Botany 36(7): e01838. https://doi.org/10.1111/njb.01838

Liu YL, Zhu XX, Peng YL, Tang M (2021) *Synotis jinshajiangensis* (Asteraceae: Senecioneae), a new species from northwestern Yunnan, China. Phytotaxa 478(1): 162–170. https://doi.org/10.11646/phytotaxa.478.1.12

Liu X, Luo JJ, Chen H, Li TY, Qu TM, Tang M, Fu ZX (2024) Comparative analysis of complete chloroplast genomes of *Synotis* species (Asteraceae, Senecioneae) for identification and phylogenetic analysis. BMC Genomics 25: 769. https://doi.org/10.1186/s12864-024-10663-x

Minh BQ, Nguyen MAT, von Haeseler A (2013) Ultrafast approximation for phylogenetic bootstrap. Molecular Biology and Evolution 30(5): 1188–1195. https://doi.org/10.1093/molbev/mst024

Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ (2015) IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Molecular Biology and Evolution 32(1): 268–274. https://doi.org/10.1093/molbev/msu300

Nordenstam B (2007) Tribe Senecioneae. In: Kadereit JW, Jeffrey C (Eds) The Families and Genera of vascular Plants, VIII. SpringerVerlag, Berlin and Heidelberg, 208–241.

Pelser PB, Nordenstam B, Kadereit J, Watson L (2007) An ITS phylogeny of tribe Senecioneae (Asteraceae) and a new delimitation of *Senecio* L. Taxon 56(4): 1077–1104. https://doi.org/10.2307/25065905

Pelser PB, Kennedy AH, Tepe EJ, Shidler JB, Nordenstam B, Kadereit JW, Watson LE (2010) Patterns and causes of incongruence between plastid and nuclear Senecioneae (Asteraceae) phylogenies. American Journal of Botany 97(5): 856–873. https://doi.org/10.3732/ajb.0900287

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Huelsenbeck JP (2012) MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61(3): 539–542. https://doi.org/10.1093/sysbio/sys029

Tang M (2014) A Systematic Study of the Genus *Synotis* (Compositae-Senecioneae). Ph.D. thesis. University of Chinese Academy of Sciences, Beijing.

Tang M, Ren C, Yang QE (2014) *Parasenecio chenopodiifolius* (Compsositae- Senecioneae) is a *Synotis* and conspecific with *S. otophylla* based on evidence from morphology, cytology and ITS/ETS sequence data. Nordic Journal of Botany 32: 824–835. https://doi.org/10.1111/njb.00574

Tang M, Hong Y, Yang QE (2013a) *Synotis baoshanensis* (Asteraceae), a new species from Yunnan, China. Botanical Studies 54: e17. https://doi.org/10.1186/1999-3110-54-17

Tang M, Wang LY, Yang QE (2013b) *Synotis xinningensis* (Asteraceae), a new species from Hunan, China. Botanical Studies 54: e16. https://doi.org/10.1186/1999-3110-54-16

Tong T, Tang M, Ren C, Yang Q (2017) *Senecio kumaonensis* (Asteraceae, Senecioneae) is a *Synotis* based on evidence from karyology and nuclear ITS/ETS sequence data. Phytotaxa 292(1): 35–46. https://doi.org/10.11646/PHYTOTAXA.292.1.3

White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (Eds) PCR Protocols: a guide to methods and applications. Academic Press, New York, 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Zhang D, Gao F, Jakovlić I, Zou H, Zhang J, Li WX, Wang GT (2020) PhyloSuite: An integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. Molecular Ecology Resources 20(1): 348–355. https://doi.org/10.1111/1755-0998.13096

Zhao LC, Chen R, Yu ZY, Tang M, Yang Q (2023) *Synotis jinpingensis* (Asteraceae, Senecioneae), a new species with white ray florets from southeastern Yunnan, China. PhytoKeys 235: 199–210. https://doi.org/10.3897/phytokeys.235.112230

Appendix 1

Table A1. Voucher information and GenBank accession of species used in our study.

GenBank No. (ITS)	Taxon	Voucher Information
–	*Synotis lhozhagensis* 01	*FLPH Expedition 24-14847* (PE)
–	*Synotis lhozhagensis* 02	*FLPH Expedition 24-14847* (PE)
–	*Synotis acuminata*	*M. Tang591* (IBSC)
–	*Synotis glomerata*	*M. Tang181* (IBSC)
–	*Synotis jinpingensis*	*Y. Yu et al. JXAU01* (JXAU)
–	*Synotis cavaleriei*	*L.Y. Wang 72* (IBSC)
AF459922	*Synotis nagensium*	*B. Bartholomew et al. 1991* (-)
AY723255	*Synotis lucorum*	*J.Q. Liu 2177* (HNWP)
EF538402	*Synotis cappa*	*Tessier-Yandell 86* (L)
KU696133	*Synotis erythropappa*	*C. Ren 150* (IBSC)
KU696135	*Synotis muliensis*	*C. Ren 148* (BSC)
KY347902	*Synotis penninervis*	*M. Tang & C. Ren 626* (BSC)
MH371137	*Synotis atractylidifolia*	*M. Tang & L. Wang 361* (IBSC)
MH371138	*Synotis karelinioides*	*H.M. Li& O.G. Mao 325* (IBSC)
KX549950	*Synotis solidaginea*	*2015XZ001-B* (IBSC)
EF538298	*Senecio arnicoide*	O. *Zollner3474* (L)
AF459925	*Senecio viscosus*	*P.B. Pelser 300* (TEX)
AF459937	*Senecio nemorensis*	*P.B. Pelser cult.102* (L)
AF459946	*Senecio doria*	*P.B. Pelser cult. 129* (WIS)
EF538222	*Senecio suaveolens*	*Elliott D.C. Dister s.n.* (MJG)
EF538298	*Senecio arnicoide*	*O. Zollner 3474* (L)
EF538312	*Senecio culcitioides*	*B. Ollgaard & H. Balslev 8822* (U)
EF538313	*Senecio chilensis*	*O. Zöllner 2958* (L)

GenBank No. (ITS)	Taxon	Voucher Information
EF538322	*Senecio ctenophyllus*	*Phil. O. Zoellner 3959* (U)
EF538348	*Senecio hypsobates*	*Wedd B. Ollgaard & H. Balslev 9863* (U)
EF538362	*Senecio oerstedianus*	*B. Nordenstam 9160* (S)
EF538373	*Senecio roseus*	*J. Garcia P. 250* (L)
GU818642	*Senecio elegans*	*Cron & Goodman 687* (-)
GU818649	*Senecio gayanus*	*M. Rosas 2157* (-)
GU818650	*Senecio gramineus*	*F.K. Hoener 2104* (-)
EF538150	*Senecio involucratus*	*B. Nordenstam 9438* (L)
GU818650	*Senecio gramineus*	*Harv. F.K. Hoener 2104* (-)
GU818662	*Senecio ilicifolius*	*Cron & Goodman 686* (-)
GU818708	*Senecio vestitus*	*P. J. Bergius W. Greuter 21766* (-)
JX895384	*Senecio scopoli* subsp. *scopolii*	–
KU499905	*Senecio changii*	*C. Ren et al. WL146* (IBSC)
KX280815	*Senecio doronicum*	*F. Schuhwerk 97/363* (M)
EF538143	*Abrotanella emarginata*	*R.N.P. Goodall & J. Wood 3352* (MU)
EF538156	*Arrhenechthites mixta*	*M.E. Lawrence 1308* (S)
EF538173	*Crassocephalum crepidioides*	*B. Nordenstam &R. Lundin 562* (S)
GU818508	*Capelio caledonica*	*B. Nordenstam 9644* (S)
GU818574	*Lachanodes arborea*	*R. Cairns-Wicks s.n.* (-)